USGS

WATER RESOURCES RESEARCH GRANT PROPOSAL

Title: Estimating the Risk of Water Contamination by Cryptosporidium parvum oocysts and other colloidal pollutants

Focus Categories: WQL, NPP, ST

Descriptors: Cryptosporidium, Solute transport, Mathematical models, Animal waste, Nonpoint source pollution

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Congressional district: 26th, NY

Critical Water Problem

Cryptosporidium parvum is a protozoan pathogen that is found in high concentrations in animal feces. It is thought that high intensity agriculture such as cattle feedlots and land application of sewage and manure may be the source of these pathogens in drinking water. There is an ever increasing interest in strategies to reduce the risk of contamination of water supplies with these types of microorganisms.

A major benefit of this project is that it will provide crucial knowledge on the risk of human exposure to C. parvum; specifically it will provide information on how both land use and environmental factors in a watershed affect the transport and viability of oocysts before they reach a water supply system. This research will also provide the means to identify populations of oocysts in soil, sediment, and raw water samples that may be less susceptible to standard disinfection treatments. It will provide a tool that can be used to quantitatively evaluate the risk of C. parvum contamination associated with agricultural and other land use practices. This information will enable city planers and environmental regulators to knowledgeably develop guidelines for the management of biological contaminants in watersheds. Additionally, this work will result in a resource that will enable water treatment managers to better determine the risks of pollution in extreme hydrologic events thereby affording them the opportunity of timely altering water treatment methods and thus avoiding the possibility of treatment failures, and outbreaks of cryptosporidiosis.

Expected Benefits/Nature, Scope, and Objectives

The primary objective of this proposed effort is to develop an accurate method for the quantitative determination of the effect of watershed management practices on the risk of human health caused by the transport of C. parvum oocysts into municipal water supplies. This goal will be achieved through development and verification of an integrated model of the transport of C. parvum oocysts in environment.

The model will have the following features:

- separation of surface from subsurface transport
- two basic modes of microorganism movement in surface flow: free advection and transport via attachment to soil articles of varying sizes
- incorporation of geographic information system to provide climate, soil, topographic and land management data
- transport of microorganisms in overland flow and their interactions with soil particles are modeled as a discrete-space continuous-time Markov process
- incorporation of first-order reliability methods to estimate the risk of water contamination and to assess the effect of environmental and management factors on the risk of contamination

To verify the model, we will

- carry out plot experiments with various vegetation, slope and soil types
- analyze the microorganism partitioning in water, soil, and sediments of varying sizes
- employ the quantitative form of polymerase chain reaction (PCR) method to estimate microorganism concentrations in water, soil, and sediments

While the proposal considers C. parvum, the methodology developed is a general approach that can accommodate many types of microbiological pathogens and colloidal pollutants.

The extent of pathogenic contamination in water catchments is influenced by many factors. These include climate, soil type, contamination source, land management, soil chemistry [24]. Baxter-Potter and Gilliland [1] reviewed studies of bacterial runoff from agricultural lands including research that showed that bacterial concentrations are highest in storm discharge and that concentrations depend on temperature, proximity of sources to rivers, livestock density and proximity, wildlife activity, fecal deposit age and channel and bank storage. A predictive model of microorganism concentrations in runoff should include these factors.

A model of water contamination from microorganisms will share many features with models of chemical contaminant transport. There are many models available of contaminant transport in watersheds (recent papers on these include [9], [27], [35], [13], [41], [12]. A review of available models can be found in [24].

Few models have been applied directly to bacterial transport. McElroy et al. [19] describe the concentration of bacteria in runoff from feedlots using the equation Y = 0.1QCDA where is the bacterial yield (organisms/d), Q is the direct runoff (cm/d), C is the concentration of bacteria in runoff (organisms/liter), D is the delivery ratio (estimated coefficient depending on the distance between livestock and the feeding stream), and A is the area of the livestock facility (ha). The runoff is estimated in [19] using the Soil Conservation Service method or an empirical regression between rainfall and runoff. In the model, the concentration of bacteria in runoff is determined by using values published in the literature. While this approach is quite reasonable given the paucity of available data, the approach does not supply any information on the temporal and spatial distribution of the runoff and so provides little help in improving management practices that are dependant upon identification of this variability.

Another limitation of many existing models is that instead of directly predicting water contamination with pathogenic microorganisms, indicator microorganisms, such as total coliforms, fecal coliforms and fecal streptococci have been used due to economical and methodological reasons [21]. However, the relationship between indicator and pathogenic microorganism populations is often not accurately determined which may lead to errors in assessment of the actual concentration of pathogens in runoff.

It is widely known that microorganisms and particularly viruses may form bonds with soil sediments [24]. Therefore, transport of microorganisms from soils is likely to be closely correlated with soil erosion and sediment transport. On the other hand, [18] showed that a significant amount of oocysts transported with overland flow are not adsorbed onto soil particles. Therefore, we consider two modes of microorganism transport: microorganisms attached to soil particles and microorganisms freely suspended in water flow. Currently formulated models describing microorganism yield in runoff [19], [21] do not make this distinction and estimate the total microorganism yield directly.

Our modeling approach will incorporate features that currently available models are lacking, such as:

1. ability to predict low probability events

2. temporal and spatial distribution of pathogenic microorganisms in runoff

3. pathogenic microorganism partitioning in soil, sediments, and the aqueous phase

4. sensitivity analysis of microorganism yield with respect to land management and environmental factors In addition, to verify the model, we will carry out a series of experiments to measure the partitioning of microorganisms in soil, sediments, and the aqueous phase.